WEST

Generate Collection

L5: Entry 1 of 4 File: USPT Apr 3, 2001

DOCUMENT-IDENTIFIER: US 6210896 B1
TITLE: Molecular motors

BSPR:
Methods to improve the output of sequence information using the Sanger method also have been proposed. These Sanger-based methods include multiplex sequencing, capillary gel electrophoresis, and automated gel electrophoresis. Recently, there has also been increasing interest in developing Sanger independent methods as well. Sanger independent methods use a completely different methodology to realize the nucleotide information. This category contains the most novel techniques, which include scanning electron microscopy (STM), mass spectrometry, enzymatic luminometric inorganic pyrophosphate detection assay (ELIDA) sequencing, exonuclease sequencing, and sequencing by hybridization.

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End of Result Set

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L5: Entry 4 of 4 File: USPT Mar 14, 2000

DOCUMENT-IDENTIFIER: US 6036923 A
TITLE: Pressure cycling reactor and methods of controlling reactions using pressure

DEPR:
2. Use of a mass spectrometer detector could also involve having only two of the four dNTPs present in the reaction chamber at the same time. Again a thio group can be incorporated into one of the dNTPs to permit identification of the source of the pyrophosphate product. This format would be slower because it would necessitate washing two different dNTP solutions in and out of the reaction chamber. There are two reasons for choosing this format; a) it would provide an additional control on the polymerase activity; and b) it provides a method for improving the yield of product for each base addition (i.e., it improves the step efficiency). The following strategy could be used to increase step efficiency. The reaction chamber could be pulsed a number of times which would equal the number of times that bases had been added from the current dNTP solution. This would allow the yield for each addition to be improved as the polymerase would be given two chances to add the base. This improvement in efficiency might allow sequencing of nucleic acids containing 10,000 or more base pairs.

FILE 'HOME' ENTERED AT 13:59:37 ON 03 JUL 2001)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, GENBANK' ENTERED AT 14:00:59 ON 03
JUL 2001

L1 0 S MICROFABRICAT? (W)SYNTHESIS(W)CHANNEL?
L2 7 S MICROFABRICAT? (P)SYNTHES? (P)CHANNEL?
L3 3 S L2 (P)(NUCLEIC OR DNA OR POLYNUCLEOTIDE? OR RNA)
L4 3 DUPLICATE REMOVE L3 (0 DUPLICATES REMOVED)